

Database : GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sts:*
- 28: em_un:*
- 29: em_vi:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htg_mus:*
- 34: em_htg_pln:*
- 35: em_htg_rod:*
- 36: em_htg_mam:*
- 37: em_htg_vrt:*
- 38: em_sy:*
- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | DB | ID | Description |
|---------------|-------|------------|--------|----|----------|---|
| | | Match | Length | | | |
| 1 | 2925 | 100.0 | 2925 | 6 | BD265755 | } <i>apparent</i> BD265755 New metal |
| 2 | 2925 | 100.0 | 2925 | 6 | AX033272 | |
| 3 | 2925 | 100.0 | 2925 | 10 | AF176569 | <i>2000</i> AF176569 Mus muscu |
| 4 | 2852 | 97.5 | 2892 | 6 | AR306357 | <i>2003</i> AR306357 Sequence |
| 5 | 2852 | 97.5 | 2892 | 6 | BD062349 | <i>2002</i> BD062349 Membrane- |

| | | | | | |
|----|--------|------|------|----|----------|
| 6 | 2852 | 97.5 | 2892 | 10 | AF157105 |
| 7 | 2704 | 92.4 | 2823 | 6 | AR306358 |
| 8 | 2704 | 92.4 | 2823 | 6 | BD062350 |
| 9 | 2610 | 89.2 | 2652 | 10 | AF302076 |
| 10 | 2483.6 | 84.9 | 2601 | 10 | AF157106 |
| 11 | 2462 | 84.2 | 2583 | 10 | AF302075 |
| 12 | 2341 | 80.0 | 2694 | 10 | AF302077 |
| 13 | 2284.2 | 78.1 | 2765 | 6 | AX014701 |
| 14 | 2284.2 | 78.1 | 2765 | 6 | BD204629 |
| 15 | 1612.8 | 55.1 | 2850 | 6 | AX747891 |
| 16 | 1612.8 | 55.1 | 2850 | 9 | AK093058 |
| 17 | 1612.8 | 55.1 | 2893 | 6 | AX356951 |
| 18 | 1612.8 | 55.1 | 2893 | 6 | AX463057 |
| 19 | 1612.8 | 55.1 | 2893 | 6 | AX665155 |
| 20 | 1612.8 | 55.1 | 2893 | 6 | AX794730 |
| 21 | 1612.8 | 55.1 | 2975 | 6 | AX356955 |
| 22 | 1612.8 | 55.1 | 2975 | 6 | AX463058 |
| 23 | 1612.8 | 55.1 | 2975 | 6 | AX665159 |
| 24 | 1612.8 | 55.1 | 2975 | 6 | AX794731 |
| 25 | 1611.2 | 55.1 | 2953 | 6 | AX473100 |
| 26 | 1607.4 | 55.0 | 2714 | | |

11/1991

| | |
|----------|-----------|
| AF157105 | Mus muscu |
| AR306358 | Sequence |
| BD062350 | Membrane- |
| AF302076 | Mus muscu |
| AF157106 | Mus muscu |
| AF302075 | Mus muscu |
| AF302077 | Mus muscu |
| AX014701 | Sequence |
| BD204629 | Novel mem |
| AX747891 | Sequence |
| AK093058 | Homo sapi |
| AX356951 | Sequence |
| AX463057 | Sequence |
| AX665155 | Sequence |
| AX794730 | Sequence |
| AX356955 | Sequence |
| AX463058 | Sequence |
| AX665159 | Sequence |
| AX794731 | Sequence |
| AX473100 | Sequence |

Database : N_Geneseq_29Jan04:*
 1: geneseqn1980s:*
 2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002s:*
 7: geneseqn2003as:*
 8: geneseqn2003bs:*
 9: geneseqn2003cs:*
 10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | % | | | | | | | | | |
|--------|--------|-------|--------|----|----------|--------------------|--|--|--|--|--|
| Result | | Query | | | | | | | | | |
| No. | Score | Match | Length | DB | ID | Description | | | | | |
| ----- | | | | | | | | | | | |
| 1 | 2925 | 100.0 | 2925 | 3 | AAA63763 | Aaa63763 cDNA enco | | | | | |
| 2 | 2284.2 | 78.1 | 2765 | 2 | AAZ28810 | Aaz28810 Rat membr | | | | | |
| 3 | 1840.6 | 62.9 | 2286 | 6 | AAD28130 | Aad28130 Soluble s | | | | | |
| 4 | 1612.8 | 55.1 | 2850 | 9 | ADB63262 | Adb63262 Human cDN | | | | | |
| 5 | 1612.8 | 55.1 | 2893 | 6 | AAD28544 | Aad28544 Human sol | | | | | |
| 6 | 1612.8 | 55.1 | 2893 | 6 | ABN84279 | Abn84279 Human SEP | | | | | |
| 7 | 1612.8 | 55.1 | 2893 | 8 | ADB61387 | Adb61387 cDNA of h | | | | | |
| 8 | 1612.8 | 55.1 | 2975 | 6 | AAD28547 | Aad28547 Human SEP | | | | | |
| 9 | 1612.8 | 55.1 | 2975 | 8 | ADB61388 | Adb61388 Human sol | | | | | |
| 10 | 1611.2 | 55.1 | 2953 | 6 | ABK48251 | Abk48251 cDNA enco | | | | | |
| 11 | 1607.4 | 55.0 | 2714 | 4 | AAF59659 | Aaf59659 Human nep | | | | | |

Database : EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| SUMMARIES | | | | | | | |
|-----------|-------|-------|-------|--------|----|----------|--------------------|
| Result | % | | | | | | Description |
| No. | Score | Query | Match | Length | DB | ID | |
| | 1 | 662.2 | 22.6 | 2253 | 29 | AY413138 | AY413138 Mus muscu |
| | 2 | 662.2 | 22.6 | 3693 | 11 | AK033824 | AK033824 Mus muscu |
| | 3 | 662.2 | 22.6 | 4241 | 11 | AK031446 | AK031446 Mus muscu |
| | 4 | 652 | 22.3 | 678 | 13 | BY747982 | BY747982 BY747982 |
| | 5 | 649.4 | 22.2 | 2253 | 29 | AY413136 | AY413136 Homo sapi |
| | 6 | 645 | 22.1 | 2253 | 29 | AY413137 | AY413137 Pan trogl |
| c | 7 | 642 | 21.9 | 704 | 12 | BG153322 | BG153322 nag12d11. |
| | 8 | 640.8 | 21.9 | 3320 | 11 | AK076908 | AK076908 Mus muscu |
| | 9 | 587.6 | 20.1 | 595 | 14 | CF106429 | CF106429 maj06g12. |
| | 10 | 542 | 18.5 | 600 | 12 | BI989738 | BI989738 4044-75 M |
| | 11 | 525.2 | 18.0 | 625 | 13 | BY727098 | BY727098 BY727098 |
| | 12 | 425.2 | 14.5 | 439 | 13 | BY463004 | BY463004 BY463004 |
| | 13 | 396.4 | 13.6 | 402 | 13 | BY533520 | BY533520 BY533520 |
| | 14 | 395.8 | 13.5 | 424 | 13 | BY454450 | BY454450 BY454450 |
| c | 15 | 391.4 | 13.4 | 507 | 10 | BE106100 | BE106100 UI-R-BO1- |
| | 16 | 382.2 | 13.1 | 419 | 13 | BY446300 | BY446300 BY446300 |
| | 17 | 381.8 | 13.1 | 400 | 13 | BY533195 | BY533195 BY533195 |

| | | | | | |
|----|-------|------|-----|----|----------|
| 18 | 380.2 | 13.0 | 395 | 13 | BY523048 |
| 19 | 378 | 12.9 | 378 | 9 | AA146423 |
| 20 | 376 | 12.9 | 401 | 13 | |

BY523048 BY523048
AA146423 mr66e08.r

Database : A_Geneseq_29Jan04:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | % | | | | | | |
|--------|--------|-------|--------|----|----------|--|--------------------|--|
| Result | | Query | | | | | | |
| No. | Score | Match | Length | DB | ID | | Description | |
| <hr/> | | | | | | | | |
| 1 | 4042 | 100.0 | 765 | 3 | AAB08130 | | Aab08130 A murine | |
| 2 | 3677 | 91.0 | 774 | 2 | AAY44177 | | Aay44177 Rat membr | |
| 3 | 3523 | 87.2 | 746 | 5 | AAE17781 | | Aae17781 Soluble s | |
| 4 | 3252.5 | 80.5 | 770 | 3 | AAB08131 | | Aab08131 A human n | |
| 5 | 3252.5 | 80.5 | 779 | 5 | AAE17779 | | Aae17779 Human sol | |
| 6 | 3252.5 | 80.5 | 779 | 5 | ABB79521 | | Abb79521 Human SEP | |
| 7 | 3252.5 | 80.5 | 779 | 5 | AAU78850 | | Aau78850 Novel nep | |
| 8 | 3252.5 | 80.5 | 779 | 7 | ADB61389 | | Adb61389 Human sol | |
| 9 | 3251.5 | 80.4 | 779 | 4 | AAB83841 | | Aab83841 Amino aci | |
| 10 | 3251.5 | 80.4 | 779 | 6 | AAE33307 | | Aae33307 Human met | |
| 11 | 3250.5 | 80.4 | 779 | 7 | ADB65232 | | Adb65232 Human pro | |
| 12 | 3249.5 | 80.4 | 779 | 4 | AAB60561 | | Aab60561 Human nep | |
| 13 | 3195.5 | 79.1 | 753 | 4 | AAB83842 | | Aab83842 Amino aci | |
| 14 | 3195.5 | 79.1 | 753 | 6 | AAE33308 | | Aae33308 Human met | |
| 15 | 3193.5 | 79.0 | 753 | 4 | AAB60562 | | Aab60562 Human nep | |
| 16 | 3156.5 | 78.1 | 742 | 5 | AAE19176 | | Aae19176 Human pro | |

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | | % | | | | | |
|--------|--------|-------|-------|--------|--------------------|-------------------|--|
| No. | Score | Query | Match | Length | ID | Description | |
| 1 | 4042 | 100.0 | 765 | 12 | US-10-267-502-257 | Sequence 257, App | |
| 2 | 3252.5 | 80.5 | 770 | 12 | US-10-267-502-251 | Sequence 251, App | |
| 3 | 3252.5 | 80.5 | 779 | 9 | US-09-905-846-2 | Sequence 2, Appli | |
| 4 | 3252.5 | 80.5 | 779 | 12 | US-10-423-543-58 | Sequence 58, Appl | |
| 5 | 3252.5 | 80.5 | 779 | 12 | US-09-928-531-2 | Sequence 2, Appli | |
| 6 | 3252.5 | 80.5 | 779 | 14 | US-10-017-273A-6 | Sequence 6, Appli | |
| 7 | 3252.5 | 80.5 | 779 | 15 | US-10-192-407C-2 | Sequence 2, Appli | |
| 8 | 3251.5 | 80.4 | 779 | 14 | US-10-147-928-4 | Sequence 4, Appli | |
| 9 | 3251.5 | 80.4 | 779 | 16 | US-10-715-112-4 | Sequence 4, Appli | |
| 10 | 3250.5 | 80.4 | 779 | 15 | US-10-104-047-3386 | Sequence 3386, Ap | |
| 11 | 3195.5 | 79.1 | 753 | 14 | US-10-147-928-6 | Sequence 6, Appli | |
| 12 | 3195.5 | 79.1 | 753 | 16 | US-10-715-112-6 | Sequence 6, Appli | |
| 13 | 3156.5 | 78.1 | 742 | 15 | US-10-274-639-13 | Sequence 13, Appl | |
| 14 | 3156.5 | 78.1 | 742 | 16 | US-10-333-574-13 | Sequence 13, Appl | |

Database : PIR_78:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % | | DB | ID | Description |
|---------------|--------|-------|--------------|----|--------|--------------------|
| | | Query | Match Length | | | |
| 1 | 3677 | 91.0 | 774 | 2 | JC7265 | neprilysin (EC 3.4 |
| 2 | 2124 | 52.5 | 750 | 1 | HYHUN | neprilysin (EC 3.4 |
| 3 | 2124 | 52.5 | 750 | 1 | HYRTN | neprilysin (EC 3.4 |
| 4 | 2108.5 | 52.2 | 751 | 1 | HYRBN | neprilysin (EC 3.4 |
| 5 | 1491 | 36.9 | 754 | 2 | A53679 | endothelin convert |
| 6 | 1490 | 36.9 | 758 | 2 | JC2521 | endothelin convert |
| 7 | 1490 | 36.9 | 770 | 2 | JC4136 | endothelin convert |
| 8 | 1485 | 36.7 | 758 | 2 | A54667 | endothelin convert |
| 9 | 1483 | 36.7 | 754 | 2 | S47268 | endothelin-convert |
| 10 | 1381.5 | 34.2 | 825 | 2 | I46078 | endothelin convert |
| 11 | 1335.5 | 33.0 | 750 | 2 | D88082 | protein T05A8.4 [i |
| 12 | 1140.5 | 28.2 | 766 | 2 | T20003 | hypothetical prote |
| 13 | 1090.5 | 27.0 | 590 | 2 | C88099 | protein F18A12.8 [|
| 14 | 1056 | 26.1 | 769 | 2 | T24949 | hypothetical prote |
| 15 | 943.5 | 23.3 | 754 | 2 | T16182 | hypothetical prote |
| 16 | 807.5 | 20.0 | 706 | 2 | F87683 | peptidase M13 fami |
| 17 | 803 | 19.9 | 700 | 2 | B82788 | metallopeptidase X |

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | | % | | | | | |
|--------|--------|-------|-------|--------|------------|--------|-------------|
| No. | Score | Query | Match | Length | DB | ID | Description |
| 1 | 2131 | 52.7 | 749 | 1 | NEP_MOUSE | Q61391 | mus musculu |
| 2 | 2124 | 52.5 | 749 | 1 | NEP_HUMAN | P08473 | homo sapien |
| 3 | 2124 | 52.5 | 749 | 1 | NEP_RAT | P07861 | rattus norv |
| 4 | 2119 | 52.4 | 749 | 1 | NEP_RABIT | P08049 | oryctolagus |
| 5 | 1491.5 | 36.9 | 762 | 1 | ECE1_RAT | P42893 | rattus norv |
| 6 | 1490 | 36.9 | 770 | 1 | ECE1_HUMAN | P42892 | homo sapien |
| 7 | 1487 | 36.8 | 754 | 1 | ECE1_CAVPO | P97739 | cavia porce |
| 8 | 1483 | 36.7 | 754 | 1 | ECE1_BOVIN | P42891 | bos taurus |
| 9 | 1430.5 | 35.4 | 787 | 1 | ECE2_HUMAN | O60344 | homo sapien |
| 10 | 1381.5 | 34.2 | 787 | 1 | ECE2_BOVIN | Q10711 | bos taurus |
| 11 | 1378.5 | 34.1 | 749 | 1 | PEX_MOUSE | P70669 | mus musculu |
| 12 | 1377.5 | 34.1 | 749 | 1 | PEX_HUMAN | P78562 | homo sapien |
| 13 | 1262 | 31.2 | 775 | 1 | ECEL_HUMAN | O95672 | homo sapien |
| 14 | 1253.5 | 31.0 | 775 | 1 | ECEL_MOUSE | Q9jmi0 | mus musculu |

Database : SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | No. | Score | % Query Match | Length | DB | ID | Description |
|--------|-----|--------|------------------|--------|----|--------|--------------------|
| | 1 | 4042 | 100.0 | 765 | 11 | Q9JLI3 | Q9jli3 mus musculu |
| | 2 | 4028 | 99.7 | 765 | 11 | Q9QZV7 | Q9qzv7 mus musculu |
| | 3 | 3900.5 | 96.5 | 742 | 11 | Q9ERK3 | Q9erk3 mus musculu |
| | 4 | 3886.5 | 96.2 | 742 | 11 | Q9QZV6 | Q9qzv6 mus musculu |
| | 5 | 3872 | 95.8 | 779 | 11 | Q9ERK2 | Q9erk2 mus musculu |
| | 6 | 3252.5 | 80.5 | 770 | 4 | Q96PH9 | Q96ph9 homo sapien |
| | 7 | 2140 | 52.9 | 750 | 11 | Q8K251 | Q8k251 mus musculu |
| | 8 | 1925.5 | 47.6 | 770 | 13 | O93394 | O93394 perca flave |
| | 9 | 1514 | 37.5 | 849 | 5 | Q9W436 | Q9w436 drosophila |
| | 10 | 1490 | 36.9 | 758 | 6 | Q28868 | Q28868 bos taurus |
| | 11 | 1485 | 36.7 | 758 | 6 | Q28010 | Q28010 bos taurus |
| | 12 | 1481 | 36.6 | 727 | 5 | Q8IS64 | Q8is64 locusta mig |
| | 13 | 1460.5 | 36.1 | 752 | 13 | Q7ZTK3 | Q7ztk3 xenopus lae |
| | 14 | 1455 | 36.0 | 752 | 13 | Q9DGN6 | Q9dgn6 gallus gall |
| | 15 | 1431 | 35.4 | 811 | 4 | Q8NFD7 | Q8nfd7 homo sapien |
| | 16 | 1413.5 | 35.0 | 763 | 11 | Q923T6 | Q923t6 mus musculu |
| | 17 | 1411.5 | 34.9 | 976 | 5 | Q9I7I4 | Q9i7i4 drosophila |
| | 18 | 1411.5 | 34.9 | 1040 | 5 | Q8T062 | Q8t062 drosophila |

09JLI3

```

ID      Q9JLI3          PRELIMINARY;          PRT;          765 AA.
AC      Q9JLI3;
DT      01-OCT-2000 (TrEMBLrel. 15, Created)
DT      01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Neprilysin-like metallopeptidase 1 (Neprilysin-like peptidase
DE      beta).
GN      MELL1 OR SEP OR NL1.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Testis;
RX      PubMed=10749671;
RA      Ghaddar G., Ruchon A.F., Carpentier M., Marcinkiewicz M., Seidah N.G.,
RA      Crine P., DesGroseillers L., Boileau G.;
RT      "Molecular cloning and biochemical characterization of a new mouse
RT      testis soluble zinc-metallopeptidase of the neprilysin family.";
RL      Biochem. J. 347:419-429(2000).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Shirotani K., Saido T.C.;
RT      "Cloning of neprilysin-like peptidase cDNAs.";
RL      Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AF176569; AAF69247.1; -.
DR      EMBL; AF302076; AAG18447.1; -.
DR      HSSP; P08473; 1DMT.
DR      MEROPS; M13.008; -.
DR      MGD; MGI:1351603; Mell1.
DR      GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR      GO; GO:0005794; C:Golgi apparatus; IDA.
DR      InterPro; IPR000718; Peptidase_M13.
DR      InterPro; IPR008753; Peptidase_M13_N.
DR      InterPro; IPR006025; Pept_M_Zn_BS.
DR      Pfam; PF01431; Peptidase_M13; 1.
DR      Pfam; PF05649; Peptidase_M13_N; 1.
DR      PRINTS; PR00786; NEPRILYSIN.
DR      PROSITE; PS00142; ZINC_PROTEASE; 1.
SQ      SEQUENCE      765 AA;  88699 MW;  D3662F1CE5B957F7 CRC64;

Query Match          100.0%;  Score 4042;  DB 11;  Length 765;
Best Local Similarity 100.0%;  Pred. No. 2.5e-237;
Matches 765;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY      1 MVERAGWCRKKSPGFVEYGLMVLLLLLLGAIIVTLGVFYSIGKQLPLLTSLLHFSWDERTV 60
Db      1 MVERAGWCRKKSPGFVEYGLMVLLLLLLGAIIVTLGVFYSIGKQLPLLTSLLHFSWDERTV 60

QY      61 VKRALRDSSLKSDICTTPSCVIAAARILENMDQSRNPCENFYQYACGGWLRHHVIPETNS 120
Db      61 VKRALRDSSLKSDICTTPSCVIAAARILENMDQSRNPCENFYQYACGGWLRHHVIPETNS 120

QY      121 RYSVFDILRDELEVILKGVLEDSTSQHRPAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLK 180

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| | | | |
|----|-----|--|-----|
| Db | 121 | RYSVFDILRDELEVILKGVLEDSTSQHRPAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLK | 180 |
| Qy | 181 | MVGGWPVAMDKWNETMGLKWELERQLAVLNSQFNRRVLIDLFIWNDDQNSSRHVIYIDQP | 240 |
| Db | 181 | MVGGWPVAMDKWNETMGLKWELERQLAVLNSQFNRRVLIDLFIWNDDQNSSRHVIYIDQP | 240 |
| Qy | 241 | TLGMPsREYYFQEDNNHKVRKAYLEFMTSVATMLRKDQNLskESAMVREEMAeVLELETH | 300 |
| Db | 241 | TLGMPsREYYFQEDNNHKVRKAYLEFMTSVATMLRKDQNLskESAMVREEMAeVLELETH | 300 |
| Qy | 301 | LANATVPQEKRHdVTALYHRMDLMELQERFGLKGFNWTLFIQNVLSSVEVELFPDEEVVV | 360 |
| Db | 301 | LANATVPQEKRHdVTALYHRMDLMELQERFGLKGFNWTLFIQNVLSSVEVELFPDEEVVV | 360 |
| Qy | 361 | YGIPYLENLEDIIDSYSARTMQNYLVWRLVLDRIgSLsQRfKEARVDYRKALYgTTVEEV | 420 |
| Db | 361 | YGIPYLENLEDIIDSYSARTMQNYLVWRLVLDRIgSLsQRfKEARVDYRKALYgTTVEEV | 420 |
| Qy | 421 | RWRECVSYVNSNMESAVGSLYIKRAFskDSKSTVRELIEKIRSVFVDNLDELNWMDEESK | 480 |
| Db | 421 | RWRECVSYVNSNMESAVGSLYIKRAFskDSKSTVRELIEKIRSVFVDNLDELNWMDEESK | 480 |
| Qy | 481 | KKAQEKAMNIREQIGYPDYILEDNNKHLDEEYSSLTfYEDLYFENGLQNLKNNaQRSLKK | 540 |
| Db | 481 | KKAQEKAMNIREQIGYPDYILEDNNKHLDEEYSSLTfYEDLYFENGLQNLKNNaQRSLKK | 540 |
| Qy | 541 | LREKVDQNLWIIGAaAVNafYSPNRNQIVFPAGILQPPFFSKDQPQSLNFGGIGMvIGHE | 600 |
| Db | 541 | LREKVDQNLWIIGAaAVNafYSPNRNQIVFPAGILQPPFFSKDQPQSLNFGGIGMvIGHE | 600 |
| Qy | 601 | ITHGFDDNGRNFDKNGNMLDwWSNfSARHFQQSQCMiYQYGNfSWELADNQNVNGFSTL | 660 |
| Db | 601 | ITHGFDDNGRNFDKNGNMLDwWSNfSARHFQQSQCMiYQYGNfSWELADNQNVNGFSTL | 660 |
| Qy | 661 | GENIADNGGVRQAYKAYLRWLADGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQ | 720 |
| Db | 661 | GENIADNGGVRQAYKAYLRWLADGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQ | 720 |
| Qy | 721 | SIKTDVHSPLKYRVLGSLQNLPGFSEAFHCPRGSPMHPMKRCRIW | 765 |
| Db | 721 | SIKTDVHSPLKYRVLGSLQNLPGFSEAFHCPRGSPMHPMKRCRIW | 765 |

RESULT 2

Q9QZV7

ID Q9QZV7 PRELIMINARY; PRT; 765 AA.
AC Q9QZV7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Soluble secreted endopeptidase.
GN MELL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20011457; PubMed=10542292;
 RA Ikeda K., Emoto N., Raharjo S.B., Nurhantari Y., Saiki K.,
 RA Yokoyama M., Matsuo M.;
 RT "Molecular identification and characterization of novel membrane-bound
 RT metalloprotease, the soluble secreted form of which hydrolyzes a
 RT variety of vasoactive peptides.";
 RL J. Biol. Chem. 274:32469-32477(1999).
 DR EMBL; AF157105; AAF13152.1; -.
 DR HSSP; P08473; 1DMT.
 DR MEROPS; M13.008; -.
 DR MGD; MGI:1351603; Mell1.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO; GO:0005794; C:Golgi apparatus; IDA.
 DR InterPro; IPR000718; Peptidase_M13.
 DR InterPro; IPR008753; Peptidase_M13_N.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR Pfam; PF01431; Peptidase_M13; 1.
 DR Pfam; PF05649; Peptidase_M13_N; 1.
 DR PRINTS; PR00786; NEPRILYSIN.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 SQ SEQUENCE 765 AA; 88651 MW; 567D3C17764C0F3F CRC64;

November 5, 1999

Query Match 99.7%; Score 4028; DB 11; Length 765;
 Best Local Similarity 99.6%; Pred. No. 1.8e-236;
 Matches 762; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| QY | 1 | MVERAGWCRKKSPGFVEYGLMVL | 60 |
| | | | |
| Db | 1 | MVERAGWCRKKSPGFVEYGLMVL | 60 |
| | | | |
| QY | 61 | VKRALRDSSLKSDICTTPSCVIAAARILENMDQSRNPCENFYQYACGGWLRHHVIPETNS | 120 |
| | | | |
| Db | 61 | VKRALRDSSLKSDICTTPSCVIAAARILENMDQSRNPCENFYQYACGGWLRHHVIPETNS | 120 |
| | | | |
| QY | 121 | RYSVFDILRDELEVILKGVLEDSTSQHRPAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLK | 180 |
| | | | |
| Db | 121 | RYSVFDILRDELEVILKGVLEDSTSQHRPAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLK | 180 |
| | | | |
| QY | 181 | MVGGWPVAMDKWNETMGLKWELERQLAVLNSQFNRRVLIDLFIWNDDQNSSRHVIYIDQP | 240 |
| | | | |
| Db | 181 | MVGGWPVALDKWNETMGLKWELERQLAVLNSQFNRRVLIDLFIWNDDQNSSRHVIYIDQP | 240 |
| | | | |
| QY | 241 | TLGMPSPREYYFQEDNNHKVRKAYLEFMTSVATMLRKDQNLKESAMVREEMA EVLELETH | 300 |
| | | | |
| Db | 241 | TLGMPSPREYYFQEDNNHKVRKAYPEFMTSVATMLRKDQNLKESAMVREEMA EVLELETH | 300 |
| | | | |
| QY | 301 | LANATVPQEKRDVTALYHRMDLMELQERFGLKGFNWTLFIQNVLSSEVELFPDEEVVV | 360 |
| | | | |
| Db | 301 | LANATVPQEKRDVTALYHRMDLMELQERFGLKGFNWTLFIQNVLSSEVELFPDEEVVV | 360 |
| | | | |
| QY | 361 | YGIPYLENLEDIIDSYSARTMQNYLVWRLVLDRI GSLSQRFKEARVDYRKALYGT TVEEV | 420 |
| | | | |
| Db | 361 | YGIPYLENLEDIIDSYSARTMQNYLVWRLVLDRI GSLSQRFKEARVDYRKALYGT TVEEV | 420 |
| | | | |
| QY | 421 | RWRECVSYVNSNMESAVGSLYIKRAFSKDSKSTVRELIEKIRSVFVDNLDELNWMDEESK | 480 |

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Db      421  |||||RWRECVSYVNSNMESAVGSLYIKRAFSKDSKSTVRELIEKIRSVFVDNLDELNWMDEESK 480
Qy      481  KKAQEKAMNIREQIGYPDYILEDNNKHLDEEYSSLTFYEDLYFENGLQNLKNNQQRSLKK 540
Db      481  |||||KKAQEKAMNIREQIGYPDYILEDNNKHLDEEYSSLTFYEDLYFENGLQNLKNNQQRSLKK 540
Qy      541  LREKVDQNLWIIGA AVVNAFYSPNRNQIVFPAGILQPPFFSKDQPQSLNFGGIGMVGIGHE 600
Db      541  |||||LREKVDQNLWIIGA AVVNAFYSPNRNQIVFPAGILQPPFFSKDQPQSLNFGGIGMVGIGHE 600
Qy      601  ITHGFDDNGRNFDDKNGNMLDWWSNFSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSTL 660
Db      601  |||||ITHGFDDNGRNFDDKNGNMLDWWSNFSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSSL 660
Qy      661  GENIADNGGVRQAYKAYLRWLADGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQ 720
Db      661  |||||GENIADNGGVRQAYKAYLRWLADGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQ 720
Qy      721  SIKTDVHSPKLYRVLGSLQNLPGFSEAFHCPRGSPMHPMKRCRIW 765
Db      721  |||||SIKTDVHSPKLYRVLGSLQNLPGFSEAFHCPRGSPMHPMKRCRIW 765

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RESULT 3

Q9ERK3

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ID   Q9ERK3          PRELIMINARY;          PRT;          742 AA.
AC   Q9ERK3;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Neprilysin-like peptidase alpha.
GN   MELL1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21293028; PubMed=11278416;
RA   Shirotani K., Tsubuki S., Iwata N., Takaki Y., Harigaya W.,
RA   Maruyama K., Kiryu-Seo S., Kiyama H., Iwata H., Tomita T.,
RA   Iwatsubo T., Saido T.C.;
RT   "Neprilysin Degrades Both Amyloid beta Peptides 1-40 and 1-42 Most
RT   Rapidly and Efficiently among Thiorphan- and Phosphoramidon-sensitive
RT   Endopeptidases.";
RL   J. Biol. Chem. 276:21895-21901(2001).
DR   EMBL; AF302075; AAG18446.1; -.
DR   HSSP; P08473; 1DMT.
DR   MEROPS; M13.008; -.
DR   MGD; MGI:1351603; Mell1.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0005794; C:Golgi apparatus; IDA.
DR   InterPro; IPR000718; Peptidase_M13.
DR   InterPro; IPR008753; Peptidase_M13_N.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   Pfam; PF01431; Peptidase_M13; 1.

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DR Pfam; PF05649; Peptidase_M13_N; 1.
DR PRINTS; PR00786; NEPRILYSIN.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
SQ SEQUENCE 742 AA; 85993 MW; 4A44EAD211B2499F CRC64;

Query Match 96.5%; Score 3900.5; DB 11; Length 742;
Best Local Similarity 97.0%; Pred. No. 9.5e-229;
Matches 742; Conservative 0; Mismatches 0; Indels 23; Gaps 1;

| | | | | | | | | | | |
|----|-----|--------------|------------|-----------|-----------|------------|-----------|---------|---------|-----|
| Qy | 1 | MVERAGWCRKKS | PGFVEYGLMV | LLLLLL | LGAIVTLGV | FYSIGKQLPL | LLTSL | LHFSW | DERTV | 60 |
| | | | | | | | | | | |
| Db | 1 | MVERAGWCRKKS | PGFVEYGLMV | LLLLLL | LGAIVTLGV | FYSI | ----- | | | 40 |
| Qy | 61 | VKRALRDSSLK | SDICTTPSC | VIAAARILE | NMDQSRNP | CENFYQYAC | GGWLRH | HVIPET | NS | 120 |
| | | | | | | | | | | |
| Db | 41 | --- | ALRDSSLK | SDICTTPSC | VIAAARILE | NMDQSRNP | CENFYQYAC | GGWLRH | HVIPET | 97 |
| Qy | 121 | RYSVFDILR | DELEVILK | GVLEDST | SQHRPAVE | KAKTLYR | SCMNQSV | IEKRDSE | PLLSVLK | 180 |
| | | | | | | | | | | |
| Db | 98 | RYSVFDILR | DELEVILK | GVLEDST | SQHRPAVE | KAKTLYR | SCMNQSV | IEKRDSE | PLLSVLK | 157 |
| Qy | 181 | MVGGWVPVAM | DKWNETM | GLKWELER | QLAVLNS | QFNRRVL | IDLFIW | NDDQN | SSRHVI | 240 |
| | | | | | | | | | | |
| Db | 158 | MVGGWVPVAM | DKWNETM | GLKWELER | QLAVLNS | QFNRRVL | IDLFIW | NDDQN | SSRHVI | 217 |
| Qy | 241 | TLGMP | SREYYFQ | EDNNHKV | RKAYLEF | MFTSVAT | MLRKDQ | NLSKES | AMVRE | 300 |
| | | | | | | | | | | |
| Db | 218 | TLGMP | SREYYFQ | EDNNHKV | RKAYLEF | MFTSVAT | MLRKDQ | NLSKES | AMVRE | 277 |
| Qy | 301 | LANATVPQ | EKRHDVT | ALYHRMD | LMELQER | FGLKGF | NWTLFI | QNVLS | SVEVEL | 360 |
| | | | | | | | | | | |
| Db | 278 | LANATVPQ | EKRHDVT | ALYHRMD | LMELQER | FGLKGF | NWTLFI | QNVLS | SVEVEL | 337 |
| Qy | 361 | YGIPYLE | NLEDIID | SYSARTM | QNYLVW | RVLDRIG | SLSQRF | KEARV | DYRKAL | 420 |
| | | | | | | | | | | |
| Db | 338 | YGIPYLE | NLEDIID | SYSARTM | QNYLVW | RVLDRIG | SLSQRF | KEARV | DYRKAL | 397 |
| Qy | 421 | RWRECVS | YVNSNM | ESAVGSL | YIKRAF | SKDSKST | VRELIE | KIRSV | FVDNL | 480 |
| | | | | | | | | | | |
| Db | 398 | RWRECVS | YVNSNM | ESAVGSL | YIKRAF | SKDSKST | VRELIE | KIRSV | FVDNL | 457 |
| Qy | 481 | KKAQEK | AMNIRE | QIGYPDY | ILEDNN | KHLDEE | YSSLTF | YEDLY | FENGLQ | 540 |
| | | | | | | | | | | |
| Db | 458 | KKAQEK | AMNIRE | QIGYPDY | ILEDNN | KHLDEE | YSSLTF | YEDLY | FENGLQ | 517 |
| Qy | 541 | LREKVDQ | NLWIIGA | AAVNNA | FYSPNR | NQIVFP | AGILQ | PPFFS | KDQPQ | 600 |
| | | | | | | | | | | |
| Db | 518 | LREKVDQ | NLWIIGA | AAVNNA | FYSPNR | NQIVFP | AGILQ | PPFFS | KDQPQ | 577 |
| Qy | 601 | ITHGFDD | NGRNFD | KNGNML | DWWSNF | SARHFQ | QQSQCM | IYQYGN | FSWEL | 660 |
| | | | | | | | | | | |
| Db | 578 | ITHGFDD | NGRNFD | KNGNML | DWWSNF | SARHFQ | QQSQCM | IYQYGN | FSWEL | 637 |
| Qy | 661 | GENIADN | GGVRQAY | KAYLRW | LADGGK | DQRLP | GLNLTY | AQLFFI | NYAQV | 720 |
| | | | | | | | | | | |
| Db | 638 | GENIADN | GGVRQAY | KAYLRW | LADGGK | DQRLP | GLNLTY | AQLFFI | NYAQV | 697 |

QY 721 SIKTDVHSPLKYRVLGSLQNLPGFSEAFHCPRGSPMHPMKRCRIW 765
 ||||||||||||||||||
 Db 698 SIKTDVHSPLKYRVLGSLQNLPGFSEAFHCPRGSPMHPMKRCRIW 742

RESULT 4

Q9QZV6

ID Q9QZV6 PRELIMINARY; PRT; 742 AA.
 AC Q9QZV6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Soluble secreted endopeptidase delta.
 GN MELL1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20011457; PubMed=10542292;
 RA Ikeda K., Emoto N., Raharjo S.B., Nurhantari Y., Saiki K.,
 RA Yokoyama M., Matsuo M.;
 RT "Molecular identification and characterization of novel membrane-bound
 RT metalloprotease, the soluble secreted form of which hydrolyzes a
 RT variety of vasoactive peptides.";
 RL J. Biol. Chem. 274:32469-32477(1999).
 DR EMBL; AF157106; AAF13153.1; -.
 DR HSSP; P08473; 1DMT.
 DR MEROPS; M13.008; -.
 DR MGD; MGI:1351603; Mell1.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO; GO:0005794; C:Golgi apparatus; IDA.
 DR InterPro; IPR000718; Peptidase_M13.
 DR InterPro; IPR008753; Peptidase_M13_N.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR Pfam; PF01431; Peptidase_M13; 1.
 DR Pfam; PF05649; Peptidase_M13_N; 1.
 DR PRINTS; PR00786; NEPRILYSIN.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 SQ SEQUENCE 742 AA; 85945 MW; CF5FF9D982471157 CRC64;

Query Match 96.2%; Score 3886.5; DB 11; Length 742;
 Best Local Similarity 96.6%; Pred. No. 6.7e-228;
 Matches 739; Conservative 2; Mismatches 1; Indels 23; Gaps 1;

QY 1 MVERAGWCRKKSPGFVEYGLMVLLLLLLGAIIVTLGVFYISIGKQLPLLTSLHFSWDERTV 60
 ||||||||||||||||||
 Db 1 MVERAGWCRKKSPGFVEYGLMVLLLLLLGAIIVTLGVFYI----- 40
 QY 61 VKRALRDSSLKSDICTTPSCVIAAARILENMDQSRNPCENFYQYACGGWLRHHVIPETNS 120
 ||||||||||||||||||
 Db 41 ---ALRDSSLKSDICTTPSCVIAAARILENMDQSRNPCENFYQYACGGWLRHHVIPETNS 97
 QY 121 RYSVFDILRDELEVILKGVLEDSTSQHRPAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLK 180
 ||||||||||||||||||
 Db 98 RYSVFDILRDELEVILKGVLEDSTSQHRPAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLK 157

| QY | 181 | MVGGWPVAMDKWNETMGLKWELERQLAVLNSQFNRRVLIDLFIWNDDQNSSRHVIYIDQP | 240 |
|----|-----|--|-----|
| Db | 158 | MVGGWPVALDKWNETMGLKWELERQLAVLNSQFNRRVLIDLFIWNDDQNSSRHVIYIDQP | 217 |
| QY | 241 | TLGMPSREYYFQEDNNHKVRKAYLEFMTSVATMLRKDQNLSSKESAMVREEMA EVLELETH | 300 |
| Db | 218 | TLGMPSREYYFQEDNNHKVRKAYPEFMTSVATMLRKDQNLSSKESAMVREEMA EVLELETH | 277 |
| QY | 301 | LANATVPQEKRHDTVATLYHRMDLMELQERFGLKGFNWTLFIQNVLSSEVELFPDEEVVV | 360 |
| Db | 278 | LANATVPQEKRHDTVATLYHRMDLMELQERFGLKGFNWTLFIQNVLSSEVELFPDEEVVV | 337 |
| QY | 361 | YGIPYLENLEDIIDSYSARTMQNYLVWRLVLDRIIGLSQRFKEARVDYRKALYGTTVVEEV | 420 |
| Db | 338 | YGIPYLENLEDIIDSYSARTMQNYLVWRLVLDRIIGLSQRFKEARVDYRKALYGTTVVEEV | 397 |
| QY | 421 | RWRECVSYVNSNMESAVGSLYIKRAFSKDSKSTVRELIEKIRSVFVDNLDELNWMDEESK | 480 |
| Db | 398 | RWRECVSYVNSNMESAVGSLYIKRAFSKDSKSTVRELIEKIRSVFVDNLDELNWMDEESK | 457 |
| QY | 481 | KKAQEKAMNIREQIGYPDYILEDNNKHLDEEYSSLTIFYEDLYFENGLQNLKNAQRSLKK | 540 |
| Db | 458 | KKAQEKAMNIREQIGYPDYILEDNNKHLDEEYSSLTIFYEDLYFENGLQNLKNAQRSLKK | 517 |
| QY | 541 | LREKVDQNLWIIIGA AVVNAFYSPNRNQIVFPAGILQPPFFSKDQPQSLNFGGIGMVIGHE | 600 |
| Db | 518 | LREKVDQNLWIIIGA AVVNAFYSPNRNQIVFPAGILQPPFFSKDQPQSLNFGGIGMVIGHE | 577 |
| QY | 601 | ITHGFDDNGRNFDDKNGNMLDWSNFSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSTL | 660 |
| Db | 578 | ITHGFDDNGRNFDDKNGNMLDWSNFSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSSL | 637 |
| QY | 661 | GENIADNGGVRQAYKAYLRWLADGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQ | 720 |
| Db | 638 | GENIADNGGVRQAYKAYLRWLADGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQ | 697 |
| QY | 721 | SIKTDVHSPLKYRVLGSLQNLPGFSEAFHCPRGSPMHPMKRCRIW | 765 |
| Db | 698 | SIKTDVHSPLKYRVLGSLQNLPGFSEAFHCPRGSPMHPMKRCRIW | 742 |

RESULT 5

Q9ERK2

ID Q9ERK2 PRELIMINARY; PRT; 779 AA.
AC Q9ERK2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Neprilysin-like peptidase gamma.
GN MELL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21293028; PubMed=11278416;
RA Shirotani K., Tsubuki S., Iwata N., Takaki Y., Harigaya W.,
RA Maruyama K., Kiryu-Seo S., Kiyama H., Iwata H., Tomita T.,
RA Iwatsubo T., Saido T.C.;
RT "Neprilysin Degrades Both Amyloid beta Peptides 1-40 and 1-42 Most
RT Rapidly and Efficiently among Thiorphan- and Phosphoramidon-sensitive
RT Endopeptidases.";
RL J. Biol. Chem. 276:21895-21901(2001).
DR EMBL; AF302077; AAG18448.1; -.
DR HSSP; P08473; 1DMT.
DR MEROPS; M13.008; -.
DR MGD; MGI:1351603; Mell1.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0005794; C:Golgi apparatus; IDA.
DR InterPro; IPR000718; Peptidase_M13.
DR InterPro; IPR008753; Peptidase_M13_N.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF01431; Peptidase_M13; 1.
DR Pfam; PF05649; Peptidase_M13_N; 1.
DR PRINTS; PR00786; NEPRILYSIN.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
SQ SEQUENCE 779 AA; 89709 MW; 5E48CA530828584B CRC64;

Query Match 95.8%; Score 3872; DB 11; Length 779;
Best Local Similarity 92.5%; Pred. No. 5.5e-227;
Matches 742; Conservative 0; Mismatches 0; Indels 60; Gaps 2;

| | | | |
|----|-----|--|-----|
| Qy | 1 | MVERAGWCRKKSPGFVEYGLMVLLLLLLGAIIVTLGVFYSIGKQLPLLTSLHFSWDERTV | 60 |
| | | | |
| Db | 1 | MVERAGWCRKKSPGFVEYGLMVLLLLLLGAIIVTLGVFYSI----- | 40 |
| Qy | 61 | VKRALRDSSLKSDICTTPSCVIAAARILENMDQSRNPCENFYQYACGGWLRHHVIPETNS | 120 |
| | | | |
| Db | 41 | ---ALRDSSLKSDICTTPSCVIAAARILENMDQSRNPCENFYQYACGGWLRHHVIPETNS | 97 |
| Qy | 121 | RYSVFDILRDELEVILKGVLEDSTSQHRPAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLK | 180 |
| | | | |
| Db | 98 | RYSVFDILRDELEVILKGVLEDSTSQHRPAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLK | 157 |
| Qy | 181 | MVGGWPVAMDKWNETMGLKWELERQLAVLNSQFNRRVLIDLFIWNDDQNSSRHVIYIDQP | 240 |
| | | | |
| Db | 158 | MVGGWPVAMDKWNETMGLKWELERQLAVLNSQFNRRVLIDLFIWNDDQNSSRHVIYIDQP | 217 |

| | | | |
|----|-----|--|-----|
| Qy | 241 | TLGMPsREYYFQEDNNHKVRKAYLEFMTSVATMLRKDQNLskESAMVREEMAeVLELETH | 300 |
| | | | |
| Db | 218 | TLGMPsREYYFQEDNNHKVRKAYLEFMTSVATMLRKDQNLskESAMVREEMAeVLELETH | 277 |
| Qy | 301 | LANATVPQEKrHDVTALYHRMDLMELQERF----- | 330 |
| | | | |
| Db | 278 | LANATVPQEKrHDVTALYHRMDLMELQERFGLKDRVSLCSPGCPGTHSVDQAGLELGNPP | 337 |
| Qy | 331 | -----GLKGfNwTLFIQNVLSSVEVELFPDEEVVVYGIPYLENLEDIIDSYSARTMQN | 383 |
| | | | |
| Db | 338 | ASDSrVLGLKGfNwTLFIQNVLSSVEVELFPDEEVVVYGIPYLENLEDIIDSYSARTMQN | 397 |
| Qy | 384 | YLVWRLVLDRIgSLsQRfKEARVDYRKALYgTTVEEVRWRECVsYVNSNMESAVGSLYIK | 443 |
| | | | |
| Db | 398 | YLVWRLVLDRIgSLsQRfKEARVDYRKALYgTTVEEVRWRECVsYVNSNMESAVGSLYIK | 457 |
| Qy | 444 | RAFskDSKSTVRELIEKIRSVFVDNLDELNWMDEESKKKAQEKAMNIREQIGYPDYILED | 503 |
| | | | |
| Db | 458 | RAFskDSKSTVRELIEKIRSVFVDNLDELNWMDEESKKKAQEKAMNIREQIGYPDYILED | 517 |
| Qy | 504 | NNKHLDEEYSSLTfYEDLYFENGLQNLKNNaQRSLKKLREKVDQNLWIIGAAVVNAFYSP | 563 |
| | | | |
| Db | 518 | NNKHLDEEYSSLTfYEDLYFENGLQNLKNNaQRSLKKLREKVDQNLWIIGAAVVNAFYSP | 577 |
| Qy | 564 | NRNQIVFPAGILQPPFFSKDQPQSLNFGGIGMVIGHEITHGFDDNGRNFDKNGNMLDWWS | 623 |
| | | | |
| Db | 578 | NRNQIVFPAGILQPPFFSKDQPQSLNFGGIGMVIGHEITHGFDDNGRNFDKNGNMLDWWS | 637 |
| Qy | 624 | NFSARHFQQSQCMiYQYGNFSWELADNQNVNGFSTLGENIADNGGVRQAYKAYLRWLAD | 683 |
| | | | |
| Db | 638 | NFSARHFQQSQCMiYQYGNFSWELADNQNVNGFSTLGENIADNGGVRQAYKAYLRWLAD | 697 |
| Qy | 684 | GGKDQRLPGLNLTYAQlFFiNYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQNLPg | 743 |
| | | | |
| Db | 698 | GGKDQRLPGLNLTYAQlFFiNYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQNLPg | 757 |
| Qy | 744 | FSEAFHCPRGSPMHPMKRCRIW | 765 |
| | | | |
| Db | 758 | FSEAFHCPRGSPMHPMKRCRIW | 779 |